



The First Scientific Conference on Health and Medical Research in the UAE-5-6 December 2022

The role of P16 gene in the diagnosis and pathogenesis of HCC

Dalia A. Gaber^{1,2}, Olfat Shaker³, Mohamed El-Kassas⁴, Sameh Sorour⁵, and Hebatallah A. Amin⁶

¹ Medical Biochemistry & Molecular Biology Department, Faculty of Medicine, Helwan University, Cairo, Egypt.

² College of Medicine, Gulf Medical University, Ajman, UAE.

³ Medical Biochemistry & Molecular Biology Department, Faculty of Medicine, Cairo University, Egypt.

⁴ Endemic Medicine Department, Faculty of Medicine, Helwan University, Cairo, Egypt.

⁵ Biochemistry and Molecular Biology Department, Faculty of Pharmacy, Helwan University, Cairo, Egypt.

⁶ Pathology Department, Faculty of Medicine, Helwan University, Cairo, Egypt.

E-mail: dr.dalia@gmu.ac.ae

ORCID ID [0000-0003-2676-9152](https://orcid.org/0000-0003-2676-9152)

Abstract

Hepatocellular carcinoma (HCC) is a common carcinoma worldwide and a leading cause of patient's cancer-related mortality. DNA methylation plays a role in the etiology and pathogenesis of hepatocellular carcinoma (HCC).

Objective: Testing the epigenetic changes in P16 gene and analyzing its expression in HCC patients.

Methodology: 50 patients with hepatocellular cancer (HCC) and 50 healthy individuals as a control group were enrolled in this study. P16 methylation was measured in the serum of HCC patients using real-time PCR after bisulfite modification.

Results: P16 gene methylation was detected in HCC group with mean percentage of 65.50 ± 16.6 , reaching 70% in cases with progressive BCLC stages

P16 gene was noticeably under-expressed in the HCC group, which varied significantly from the control group ($p=0.0001$). The Receiver operating characteristic (ROC) curve analysis showed that both biomarkers have reliable sensitivity and specificity.

Conclusion: P16 gene had aberrant methylation in HCC cases, which was significantly enhanced in cases with child score C & advanced BCLC stage. There was an under expression of P16 gene. This gene can be considered potential diagnostic biomarkers for HCC.

Key Words: P16, aberrant methylation, HCC, genetic biomarkers.